

SEQUENCE LISTING

<110> Salter, Michael
Gingrich, Jeffrey

<120> Method for Modification of NMDA Receptors Through Inhibition of Src

<130> 2560.004

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 9

<212> PRT

<213> Homo sapiens

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Lys Pro Ala Ser Ala Asp Gly His Arg
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<210> 2

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<212> PRT

<213> Homo sapiens

<400> 2

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Asp Gly His Arg
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<210> 3

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<212> DNA

<213> Homo sapiens

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<210> 4
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 <212> PRT
 <213> Homo sapiens
 <400> 4

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Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe Pro
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Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg Gly
35 40 45

Pro Ser Ala Ala Phe Ala Pro Ala Ala Glu Pro Lys Leu Phe Gly
50 55 60

Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Pro
65 70 75 80

Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser
85 90 95

Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile
100 105 110

Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser Thr
115 120 125

Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser
130 135 140

Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser
145 150 155 160

Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu Val
165 170 175

Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp
180 185 190

Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys
195 200 205

Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn Ser
210 215 220

Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys
225 230 235 240

His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly
245 250 255

Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu
260 265 270

Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp
275 280 285

Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met
290 295 300

Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg
305 310 315 320

His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile
325 330 335

Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu
340 345 350

Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met
355 360 365

Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr
370 375 380

Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu
385 390 395 400

Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn
405 410 415

Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala
420 425 430

Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp
435 440 445

Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro
450 455 460

Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly
465 470 475 480

Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu
485 490 495

Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe Glu
500 505 510

Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln
515 520 525

Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 5
<211> 10
<212> PRT
<213> Artificial

<220>
<223> src-activating peptide, used as a control

<220>
<221> MOD_RES
<222> (4)..(4)
<223> PHOSPHORYLATION

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1 5 10

<210> 6
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<212> DNA
<213> Homo sapiens

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cccaccatca tagccaccat cacccctcctt aacctctact tctacctacg cctaattctac 180
tccacctcaa tcacactact ccccatatct aacaacgtaa aaataaaatg acagttt 237

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<211> 80
<212> PRT
<213> Homo sapiens

<400> 7

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Pro Pro Leu Thr Gly Phe Leu Pro Lys Trp Thr Ile Ile Glu Glu Phe
20 25 30

Thr Lys Asn Asn Ser Leu Ile Ile Pro Thr Ile Met Ala Thr Ile Thr
35 40 45

Leu Leu Asn Leu Tyr Phe Tyr Leu Arg Leu Ile Tyr Ser Thr Ser Ile

50

55

60

Thr Leu Leu Pro Met Ser Asn Asn Val Lys Met Lys Trp Gln Phe Glu
65 70 75 80

<210> 8

<211> 1044

<212> DNA

<213> Homo sapiens

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<210> 9

<211> 347

<212> PRT

<213> Homo sapiens

<400> 9

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Thr Leu Ile Thr Ala Leu Ser Ser His Trp Phe Phe Thr Trp Val Gly
20 25 30

Leu Glu Met Asn Met Leu Ala Phe Ile Pro Val Leu Thr Lys Lys Met
35 40 45

Asn Pro Arg Ser Thr Glu Ala Ala Ile Lys Tyr Phe Leu Thr Gln Ala
50 55 60

Thr Ala Ser Met Ile Leu Leu Met Ala Ile Leu Phe Asn Asn Met Leu
65 70 75 80

Ser Gly Gln Trp Thr Met Thr Asn Thr Thr Asn Gln Tyr Ser Ser Leu
85 90 95

Met Ile Met Met Ala Met Ala Met Lys Leu Gly Met Ala Pro Phe His
100 105 110

Phe Trp Val Pro Glu Val Thr Gln Gly Thr Pro Leu Thr Ser Gly Leu
115 120 125

Leu Leu Leu Thr Trp Gln Lys Leu Ala Pro Ile Ser Ile Met Tyr Gln
130 135 140

Ile Ser Pro Ser Leu Asn Val Ser Leu Leu Leu Thr Leu Ser Ile Leu
145 150 155 160

Ser Ile Met Ala Gly Ser Trp Gly Gly Leu Asn Gln Thr Gln Leu Arg
165 170 175

Lys Ile Leu Ala Tyr Ser Ser Ile Thr His Met Gly Trp Met Met Ala
180 185 190

Val Leu Pro Tyr Asn Pro Asn Met Thr Ile Leu Asn Leu Thr Ile Tyr
195 200 205

Ile Ile Leu Thr Thr Ala Phe Leu Leu Leu Asn Leu Asn Ser Ser
210 215 220

Thr Thr Thr Leu Leu Leu Ser Arg Thr Trp Asn Lys Leu Thr Trp Leu
225 230 235 240

Thr Pro Leu Ile Pro Ser Thr Leu Leu Ser Leu Gly Gly Leu Pro Pro
245 250 255

Leu Thr Gly Phe Leu Pro Lys Trp Ala Ile Ile Glu Glu Phe Thr Lys
260 265 270

Asn Asn Ser Leu Ile Ile Pro Thr Ile Met Ala Thr Ile Thr Leu Leu
275 280 285

Asn Leu Tyr Phe Tyr Leu Arg Leu Ile Tyr Ser Thr Ser Ile Thr Leu
290 295 300

Leu Pro Met Ser Asn Asn Val Lys Met Lys Trp Gln Phe Glu His Thr
305 310 315 320

Lys Pro Thr Pro Phe Leu Pro Thr Leu Ile Ala Leu Thr Thr Leu Leu
325 330 335

Leu Pro Ile Ser Pro Phe Met Leu Met Ile Leu
340 345

<210> 10

<211> 150

<212> DNA

<213> Homo sapiens

<400> 10

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<211> 51

<212> PRT

<213> Homo sapiens

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Trp Met Met Ala Val Leu Pro Tyr Asn Pro Asn Met Thr Ile Leu Asn
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Leu Thr Ile Tyr Ile Ile Leu Thr Thr Thr Ala Phe Leu Leu Leu Asn
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Leu Asn Ser Ser Thr Thr Thr Leu Leu Leu Ser Arg Thr Trp Asn Lys
35 40 45

Leu Thr Trp
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<210> 12

<211> 564

<212> DNA

<213> Homo sapiens

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atccagttc taaccaaaaa aataaaccct cgttccacag aagctgccat caagtatttc 180

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<211> 188
<212> PRT
<213> Homo sapiens

<400> 13

Met Asn Pro Leu Ala Gln Pro Val Ile Tyr Ser Thr Ile Phe Ala Gly
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Thr Leu Ile Thr Ala Leu Ser Ser His Trp Phe Phe Thr Trp Val Gly
20 25 30

Leu Glu Met Asn Met Leu Ala Phe Ile Pro Val Leu Thr Lys Lys Met
35 40 45

Asn Pro Arg Ser Thr Glu Ala Ala Ile Lys Tyr Phe Leu Thr Gln Ala
50 55 60

Thr Ala Ser Met Ile Leu Leu Met Ala Ile Leu Phe Asn Asn Met Leu
65 70 75 80

Ser Gly Gln Trp Thr Met Thr Asn Thr Thr Asn Gln Tyr Ser Ser Leu
85 90 95

Met Ile Met Met Ala Met Ala Met Lys Leu Gly Met Ala Pro Phe His
100 105 110

Phe Trp Val Pro Glu Val Thr Gln Gly Thr Pro Leu Thr Ser Gly Leu
115 120 125

Leu Leu Leu Thr Trp Gln Lys Leu Ala Pro Ile Ser Ile Met Tyr Gln
130 135 140

Ile Ser Pro Ser Leu Asn Val Ser Leu Leu Leu Thr Leu Ser Ile Leu
145 150 155 160

Ser Ile Met Ala Gly Ser Trp Gly Gly Leu Asn Gln Thr Gln Leu Arg
10

165

170

175

Lys Ile Leu Ala Tyr Ser Ser Ile Thr His Met Gly
180 185